PatentIn.prjSubstitute.ST25.txt
SEQUENCE LISTING

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<110> Cyclacel

<120> Compositions and Methods for Monitoring the Modification of Modification
Dependent Binding Partner Polypeptides

<130> 10069/1062

<140> 09/770102

<141> 2001-01-25

<150> US 60/179283

<151> 2000-01-31

<160> 57

<170> PatentIn version 3.1

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<211> 17

<212> PRT

<213> Unknown

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<223> ADP-ribosylation domain

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<222> (1)..(17)

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1   5   10   15

Asp

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<213>   Unknown

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<223>   ADP-ribosylation site

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1   5   10

<210>   3

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<213>   Unknown

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<223>   ubiquitination site

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Arg Asp Gly Leu Lys Lys Glu Arg Leu Leu Asp Asp Arg His
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<211> 10

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<213> Unknown

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<221> DOMAIN

<222> (1)..(10)

<223> O-GlcNAc site

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Gly Thr Thr Ser Thr Ile Gln Thr Ala Pro
1   5   10

<210> 6

<211> 12

<212> PRT

<213> Unknown

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Ser Ala Val Ser Ser Ala Asp Gly Thr Val Leu Lys
1   5   10

<210> 7

<211> 18

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<223> O-GlcNAc site

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Asp Ser Ser Thr Asp Leu Thr Gln Thr Ser Ser Ser Gly Thr Val Thr
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Leu Pro

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<211> 12

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1   5   10

<210> 9

<211> 13

<212> PRT

<213> Unknown

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Ala Gln Thr Ile Thr Ser Glu Thr Pro Ser Ser Thr Thr
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<223>   Xaa at position 6 may be any amino acid

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<222>   (1)..(8)

<223>   Xaa at position 3 may be any amino acid

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<210>   11

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<222> (1)..(5)

<223> Consensus sequence, each Xaa is any amino acid

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<222> (1)..(5)

<223> X at posistion 2, 3, and 5 can be any amino acid

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Lys Xaa Xaa Ser Xaa
1   5

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<211> 3

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<222> (1)..(3)

<223> X at posistion 2 can be any amino acid

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Arg Xaa Thr
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<210> 13

<211> 5

<212> PRT

<213> Unknown

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<220>

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<223> X at posistion 2, 3, and 5 can be any amino acid

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<210> 14

<211> 4

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<222> (1)..(4)

<223> X at posistion 1 and 4 can be any amino acid

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Xaa Ser Arg Xaa
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<211> 8

<212> PRT

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<222> (1)..(8)

<223> X at posistion 1, 3, 4, 6 and 8 can be any amino acid

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<210> 16

<211> 6

<212>   PRT

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<222>   (1)..(6)

<223>   Consensus sequence, each Xaa is any amino acid

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<222>   (1)..(6)

<223>   X at posistion 1, 3, 4, and 6 can be any amino acid

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1   5

<210>   17

<211>   6

<212>   PRT

<213>   Unknown

<220>

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<222>   (1)..(6)

<223>   Consensus sequence

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Ser Glu Leu Ser Arg Arg

1   5

<210> 18

<211> 6

<212> PRT

<213> Unknown

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<222> (1)..(6)

<223> Consensus sequence, each Xaa is any amino acid

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<222> (1)..(6)

<223> X at posistion 1,3,4, and 6 can be any amino acid

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Xaa Ser Xaa Xaa Ser Xaa
1   5

<210> 19

<211> 5

<212> PRT

<213> Unknown

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<223> Consensus sequence, each Xaa is any amino acid

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<222> (1)..(5)

<223> X at posistion 1, 3, and 5 can be any amino acid

<400> 19

Xaa Ser Xaa Glu Xaa
1   5

<210> 20

<211> 7

<212> PRT

<213> Unknown

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<223> Consensus sequence

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<221> DOMAIN

<222> (1)..(7)

<223> Consensus sequence, each Xaa is any amino acid

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<221> MISC_FEATURE

<222> (1)..(7)

<223> X at poaiation a, 3, 4, 5, and 7 can be any amino acid

<400> 20

Xaa Ser Xaa Xaa Xaa Ser Xaa
1   5

<210> 21

<211> 9

<212>   PRT

<213>   Unknown

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<223>   Consensus sequence

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<221>   DOMAIN

<222>   (1)..(9)

<223>   Consensus sequence

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Gly Ser Ser Lys Ser Lys Pro Lys Asp
1   5

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<211>   9

<212>   PRT

<213>   Unknown

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<223>   Consensus sequence

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<221>   DOMAIN

<222>   (1)..(9)

<223>   Consensus sequence

<400>   22

Gly Cys Ile Lys Ser Lys Arg Lys Asp
1   5

<210>   23

<211>   9

<212>   PRT

<213>   Unknown

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<222>   (1)..(9)

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Gly Cys Ile Lys Ser Lys Glu Asp Lys
1   5

<210>   24

<211>   9

<212>   PRT

<213>   Unknown

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<222>   (1)..(9)

<223>   Consensus sequence

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Gly Cys Val Gln Cys Lys Asp Lys Glu
1   5

<210>   25

<211>   9

<212>   PRT

<213>   Unknown

<220>

<223> Consensus sequence

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<222> (1)..(9)

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Gly Cys Thr Leu Ser Ala Glu Asp Lys
1   5

<210> 26

<211> 9

<212> PRT

<213> Unknown

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<223> Consensus sequence

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Gly Cys Ile Lys Ser Lys Arg Lys Asp
1   5

<210> 27

<211> 9

<212> PRT

<213> Unknown

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<223> Consensus sequence

<220>

<221> DOMAIN

<222> (1)..(9)

<223> Consensus sequence

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Gly Cys Val Gln Cys Lys Asp Lys Glu
1   5

<210> 28

<211> 9

<212> PRT

<213> Unknown

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<223> Consensus sequence

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<221> DOMAIN

<222> (1)..(9)

<223> Consensus sequence

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Gly Cys Thr Leu Ser Ala Glu Asp Lys
1   5

<210> 29

<211> 4

<212> PRT

<213> Unknown

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<222> (1)..(4)

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<220>

<221> MISC_FEATURE

<222> (1)..(4)

<223> X at posistion 2 can be any amino acid

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Asn Xaa Ser Thr
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<210> 30

<211> 4

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<213> Unknown

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<222> (1)..(4)

<223> C-terminal sequence

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His Ser Thr Val
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<210> 31

<211> 92

<212> DNA

<213> Artificial Sequence

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<220>

<221> misc_feature

<222> (1)..(92)

<223> Synthetic primer

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gggggggagct ctgggaggcg gaggtggagg gctgatgcgc cagctgcagg atgaagttga   60

agaactggaa caggaaaact ggcatctgca ga   92

<210> 32

<211> 96

<212> DNA

<213> Artificial Sequence

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<220>

<221> misc_feature

<222> (1)..(96)

<223> Synthetic primer

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cccccctcga gttattaaac ttcggcttcc aggcactgaa cttcacgcag cagacgggca   60

acttcgttct gcagatgcca gttttcctgt tccagt   96

<210> 33

<211> 37

<212> PRT

<213> Unknown

<220>

<223> Coiled-coil sequence

<220>

<221> DOMAIN

<222> (1)..(37)

<223> Coiled coil sequence

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Leu Met Arg Gln Leu Gln Asp Glu Val Glu Glu Leu Glu Gln Glu Asn
1   5   10   15

Trp His Leu Gln Asn Glu Val Ala Arg Leu Leu Arg Glu Val Gln Cys
                20   25   30

Leu Glu Ala Glu Val
        35

<210> 34

<211> 37

<212> PRT

<213> Unknown

<220>

<223> Coiled coil sequence

<220>

<221> DOMAIN

<222> (1)..(37)

<223> Coiled coil sequence

<400> 34

Arg Met Arg Gln Leu Glu Asp Arg Val Glu Glu Leu Arg Glu Gln Asn
1   5   10   15

Trp His Leu Ala Asn Gln Val Ala Arg Leu Arg Gln Arg Val Cys Glu
                20   25   30

Leu Lys Ala Arg Val
        35

<210> 35

<211> 80

<212> DNA

<213> Artificial Sequence

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<221> misc_feature

<222> (1)..(80)

<223> Synthetic primer

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gtaccgctag ctcttacaag ggtattgctc agttggagca ggaaatcgcc caattagaac   60

aagaaaatgc acaacttgaa   80

<210> 36

<211> 73

<212> DNA

<213> Artificial Sequence

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<223> Synthetic primer

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<221> misc_feature

<222> (1)..(61)

<223> Synthetic primer

<400> 36

gggcatcgat ttcctgctca agctgagcga tctcttgttc aagttgtgca ttttcttgtt   60

ctaattgggc gat   73

<210> 37

<211> 31

<212> PRT

<213> Unknown

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<223> Sequence for cloning

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<221> DOMAIN

<222> (1)..(31)

<223> Sequence for cloning

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Tyr Lys Gly Ile Ala Gln Leu Glu Gln Glu Ile Ala Gln Leu Glu Gln
1   5   10   15

Glu Asn Ala Gln Leu Glu Gln Glu Ile Ala Gln Leu Glu Gln Glu
            20   25   30

<210> 38

<211> 38

<212> PRT

<213> Unknown

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<223> Coiled coil sequence

<220>

<221> DOMAIN

<222> (1)..(38)

<223> Coiled coil sequence

<400> 38

Tyr Lys Gly Ile Cys Gln Leu Arg Gln Arg Ile Ala Gln Leu Arg Gln
1   5   10   15

Arg Asn Ala Gln Leu Arg Gln Arg Ile Ala Gln Leu Arg Gln Arg Ile
            20   25   30

Ala Gln Leu Arg Gln Arg
            35

<210> 39

<211> 36

<212> PRT

<213> Artificial Sequence

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<223> Synthetic peptide

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<221> PEPTIDE

<222> (1)..(36)

<223> Synthetic peptide

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Arg Cys Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly
1   5   10   15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            20   25   30

Asp Val Leu Asp
            35

<210> 40

<211> 36

<212> PRT

<213> Artificial Sequence

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<223> Synthetic peptide

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<221> PEPTIDE

<222> (1)..(36)

<223> Synthetic peptide

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Arg Cys Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly
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Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            20   25   30

Asp Val Leu Asp
        35

<210> 41

<211> 33

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<210> 42

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<223> Synthetic primer

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ggaattcggg cactgctgtt ggggcaggcc tcc   33

<210> 43

<211> 23

<212> DNA

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gggggcccag agtgaagttc agc   23

<210> 44

<211> 23

<212> DNA

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<221> misc_feature

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<400> 44
gggggcccga gcccccgcg tac   23

<210> 45

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic primer

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<221> misc_feature

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<211> 23

<212> DNA

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<221> misc_feature

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<223>   Synthetic peptide

<400>   47

Arg Cys Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly
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Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
                20   25   30

Asp Val Leu Asp
            35

<210>   48

<211>   6

<212>   PRT

<213>   Unknown

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<223>   Cleavage site

<220>

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<222>   (1)..(6)

<223>   X at posistion 6 can be any amino acid

<220>

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<222> (1)..(6)

<223> Clavage site, X can be any mino acid

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Trp Leu Glu His Asp Xaa
1   5

<210> 49

<211> 5

<212> PRT

<213> Unknown

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<223> Cleavage site

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<222> (1)..(5)

<223> Cleavage site, each Xaa is any amino acid

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<222> (1)..(5)

<223> X at posistion 3 and 5 can be any amino acid

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Asp Glu Xaa Asp Xaa
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<210> 50

<211> 6

<212> PRT

<213> Unknown

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<222> (1)..(6)

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<220>

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<222> (1)..(6)

<223> X at posistion 4 and 6 can be any amino acid

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Leu Val Glu Xaa Asp Xaa
1   5

<210> 51

<211> 5

<212> PRT

<213> Unknown

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<223> Cleavage site, Xaa is any amino acid

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> X at posistion 5 can be any amino acid

<400> 51

Ile Glu Gly Arg Xaa
1   5

<210> 52

<211> 8

<212> PRT

<213> Unknown

<220>

<223> Cleavage site

<220>

<221> SITE

<222> (1)..(8)

<223> Cleavage site, each Xaa is any amino acid

<220>

<221> MISC_FEATURE

<222> (1)..(8)

<223> X at posistion 3 and 5 can be any amino acid

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Glu Asn Xaa Tyr Xaa Gln Ser Gly
1   5

<210> 53

<211> 5

<212> PRT

<213> Artificial Sequence

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<223> Tag peptide

<220>

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<222> (1)..(5)

<223> Tag peptide

<400> 53

Arg Tyr Ile Arg Ser
1   5

<210> 54

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Tag peptide

<220>

<221> PEPTIDE

<222> (1)..(6)

<223> Tag peptide

<400> 54

Asp Thr Tyr Arg Tyr Ile
1   5

<210> 55

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Tag peptide

<220>

<221> PEPTIDE

<222> (1)..(6)

<223> Tag peptide

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Thr Asp Phe Leu Tyr Lys
1   5

<210> 56

<211> 9

<212> PRT

<213> Artificial Sequence

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<222> (1)..(9)

<223> Tag sequence

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Glu Glu Glu Glu Tyr Met Pro Met Glu
1   5

<210> 57

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Tag peptide

<220>

<221> PEPTIDE

<222> (1)..(11)

<223> Tag sequence

<400> 57

Lys Pro Pro Thr Pro Pro Pro Glu Pro Glu Thr
1   5   10